



RAW SEQUENCE LISTING ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 10/509,095
Source: PT/10
Date Processed by STIC: 10/4/04

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT MARK SPENCER, TELEPHONE: 571-272-2510; FAX: 571-273-0221

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 4.2 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:

<http://www.uspto.gov/web/offices/pac/checker/chkrnote.htm>

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.

Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.

Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<<http://www.uspto.gov/ebc/efs/downloads/documents.htm>> , EFS Submission User Manual - ePAVE)
2. U.S. Postal Service: Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450
3. Hand Carry, Federal Express, United Parcel Service, or other delivery service (EFFECTIVE 06/05/04):
U.S. Patent and Trademark Office, 220 20th Street S., Customer Window, Mail Stop Sequence, Crystal Plaza Two, Lobby, Room 1B03, Arlington, VA 22202

Revised 05/17/04

Raw Sequence Listing Error Summary

ERROR DETECTED	SUGGESTED CORRECTION	SERIAL NUMBER: <u>10/509,095</u>
ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE		
1 <input type="checkbox"/> Wrapped Nucleics Wrapped Aminos	The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."	
2 <input checked="" type="checkbox"/> Invalid Line Length	The rules require that a line not exceed 72 characters in length. This includes white spaces.	
3 <input checked="" type="checkbox"/> Misaligned Amino Numbering	The numbering under each 5 th amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.	
4 <input checked="" type="checkbox"/> Non-ASCII	The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.	
5 <input type="checkbox"/> Variable Length	Sequence(s) _____ contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.	
6 <input type="checkbox"/> PatentIn 2.0 "bug"	A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.	
7 <input type="checkbox"/> Skipped Sequences (OLD RULES)	Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence: (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown) (i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading) (xi) SEQUENCE DESCRIPTION: SEQ ID NO:X: (insert SEQ ID NO where "X" is shown) This sequence is intentionally skipped Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.	
8 <input type="checkbox"/> Skipped Sequences (NEW RULES)	Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence. <210> sequence id number <400> sequence id number 000	
9 <input type="checkbox"/> Use of n's or Xaa's (NEW RULES)	Use of n's and/or Xaa's have been detected in the Sequence Listing. Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present. In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.	
10 <input type="checkbox"/> Invalid <213> Response	Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence	
11 <input type="checkbox"/> Use of <220>	Sequence(s) _____ missing the <220> "Feature" and associated numeric identifiers and responses. Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section. (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)	
12 <input type="checkbox"/> PatentIn 2.0 "bug"	Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.	
13 <input type="checkbox"/> Misuse of n/Xaa	"n" can only represent a single nucleotide; "Xaa" can only represent a single amino acid	

see item 4 on Error Summary Sheet
 also, per 1.824) sequence Rules: a label
 needs to be placed on disk
 (see 1.824)



PCT

RAW SEQUENCE LISTING

DATE: 10/04/2004

PATENT APPLICATION: US/10/509,095

TIME: 11:05:10

Input Set : A:\PTO.FG.txt

Output Set: N:\CRF4\10042004\J509095.raw

3 <110> APPLICANT: JSW RESEARCH FORSCHUNGLABOR GMBH
 W--> 4 <120> TITLE OF INVENTION: Neurotrophic and Neuroprotective Peptides
 W--> 5 <140> CURRENT APPLICATION NUMBER: PCT/AT/03/00065
 W--> 6 <130> FILE REFERENCE:
 C--> 6 <141> CURRENT FILING DATE: 2004-09-28
 7 <150> PRIOR APPLICATION NUMBER: AT A 495/2002
 W--> 8 <151> PRIOR FILING DATE: 3/28/2002
 W--> 9 <160> NUMBER OF SEQ ID: 46
 10 <170> SOFTWARE: MS Word 2002 for Windows

see p. 6 for explanation

ERRORED SEQUENCES

Does Not Comply
 Corrected Diskette Needed

12 <210> SEQ ID NO: 1
 13 <211> LENGTH: 14
 E--> 14 <212> TYPE: Peptide PRT
 15 <213> ORGANISM: Artificial sequence
 W--> 16 <220> FEATURE:
 W--> 16 <223> OTHER INFORMATION: (400) 1 T.L. (400) line goes above the amino acids
 E--> 16 <400> SEQUENCE: Asp Val Phe Met Lys Gly Leu Ser Met Ala Lys Glu Gly Val
 17 1 5 10 misaligned amino acid numbers. see item 3 on Error Summary Sheet.
 19 <210> SEQ ID NO: 2
 20 <211> LENGTH: 12
 E--> 21 <212> TYPE: Peptide same error
 22 <213> ORGANISM: Artificial sequence
 W--> 23 <220> FEATURE:
 W--> 23 <223> OTHER INFORMATION: (400) 2
 E--> 23 <400> SEQUENCE: Val Phe Met Lys Gly Leu Ser Met Ala Lys Glu Gly Val
 24 1 5 10
 26 <210> SEQ ID NO: 3
 27 <211> LENGTH: 12
 E--> 28 <212> TYPE: Peptide same
 29 <213> ORGANISM: Artificial sequence
 W--> 30 <220> FEATURE:
 W--> 30 <223> OTHER INFORMATION:
 E--> 30 <400> SEQUENCE: Phe Met Lys Gly Leu Ser Met Ala Lys Glu Gly Val
 31 1 5 10
 33 <210> SEQ ID NO: 4
 34 <211> LENGTH: 11
 E--> 35 <212> TYPE: Peptide
 36 <213> ORGANISM: Artificial sequence
 W--> 37 <220> FEATURE:
 W--> 37 <223> OTHER INFORMATION:

RAW SEQUENCE LISTING
PATENT APPLICATION: US/10/509,095

DATE: 10/04/2004
TIME: 11:05:10

Input Set : A:\PTO.FG.txt
Output Set: N:\CRF4\10042004\J509095.raw

E--> 37 <400> SEQUENCE: Met Lys Gly Leu Ser Met Ala Lys Glu Gly Val
38 1 5 10
40 <210> SEQ ID NO: 5
41 <211> LENGTH: 10
E--> 42 <212> TYPE: Peptide
43 <213> ORGANISM: Artificial sequence
W--> 44 <220> FEATURE:
W--> 44 <223> OTHER INFORMATION:
E--> 44 <400> SEQUENCE: Lys Gly Leu Ser Met Ala Lys Glu Gly Val
45 1 5 10
47 <210> SEQ ID NO: 6
48 <211> LENGTH: 9
E--> 49 <212> TYPE: Peptide
50 <213> ORGANISM: Artificial sequence
W--> 51 <220> FEATURE:
W--> 51 <223> OTHER INFORMATION:
E--> 51 <400> SEQUENCE: Gly Leu Ser Met Ala Lys Glu Gly Val
52 1 5
54 <210> SEQ ID NO: 7
55 <211> LENGTH: 8
E--> 56 <212> TYPE: Peptide
57 <213> ORGANISM: Artificial sequence
W--> 58 <220> FEATURE:
W--> 58 <223> OTHER INFORMATION:
E--> 58 <400> SEQUENCE: Leu Ser Met Ala Lys Glu Gly Val
59 1 5
61 <210> SEQ ID NO: 8
62 <211> LENGTH: 7
E--> 63 <212> TYPE: Peptide
64 <213> ORGANISM: Artificial sequence
W--> 65 <220> FEATURE:
W--> 65 <223> OTHER INFORMATION:
E--> 65 <400> SEQUENCE: Ser Met Ala Lys Glu Gly Val
66 1 5
68 <210> SEQ ID NO: 9
69 <211> LENGTH: 6
E--> 70 <212> TYPE: Peptide
71 <213> ORGANISM: Artificial sequence
W--> 72 <220> FEATURE:
W--> 72 <223> OTHER INFORMATION:
E--> 72 <400> SEQUENCE: Met Ala Lys Glu Gly Val
73 1 5
75 <210> SEQ ID NO: 10
76 <211> LENGTH: 5
E--> 77 <212> TYPE: Peptide
78 <213> ORGANISM: Artificial sequence
W--> 79 <220> FEATURE:
W--> 79 <223> OTHER INFORMATION:
E--> 79 <400> SEQUENCE: Ala Lys Glu Gly Val

same

same
error

RAW SEQUENCE LISTING

DATE: 10/04/2004

PATENT APPLICATION: US/10/509,095

TIME: 11:05:10

Input Set : A:\PTO.FG.txt

Output Set: N:\CRF4\10042004\J509095.raw

```

80 1          5
82 <210> SEQ ID NO: 11
83 <211> LENGTH: 5 4 shown
E--> 84 <212> TYPE: Peptide
85 <213> ORGANISM: Artificial sequence
W--> 86 <220> FEATURE:
W--> 86 <223> OTHER INFORMATION:
E--> 86 <400> SEQUENCE: Lys Glu Gly Val
87 1
89 <210> SEQ ID NO: 12
90 <211> LENGTH: 14
E--> 91 <212> TYPE: Peptide
92 <213> ORGANISM: Artificial sequence
W--> 93 <220> FEATURE:
W--> 93 <223> OTHER INFORMATION:
E--> 93 <400> SEQUENCE: Met Asp Val Phe Met Lys Gly Leu Ser Met Ala Lys Glu Gly
94 1 5 10
96 <210> SEQ ID NO: 13
97 <211> LENGTH: 13
E--> 98 <212> TYPE: Peptide
99 <213> ORGANISM: Artificial sequence
W--> 100 <220> FEATURE:
W--> 100 <223> OTHER INFORMATION:
E--> 100 <400> SEQUENCE: Met Asp Val Phe Met Lys Gly Leu Ser Met Ala Lys Glu
101 1 5 10
103 <210> SEQ ID NO: 14
104 <211> LENGTH: 12
E--> 105 <212> TYPE: Peptide
106 <213> ORGANISM: Artificial sequence
W--> 107 <220> FEATURE:
W--> 107 <223> OTHER INFORMATION:
E--> 107 <400> SEQUENCE: Met Asp Val Phe Met Lys Gly Leu Ser Met Ala Lys
108 1 5 10
110 <210> SEQ ID NO: 15
111 <211> LENGTH: 11
E--> 112 <212> TYPE: Peptide
113 <213> ORGANISM: Artificial sequence
W--> 114 <220> FEATURE:
W--> 114 <223> OTHER INFORMATION:
E--> 114 <400> SEQUENCE: Met Asp Val Phe Met Lys Gly Leu Ser Met Ala
115 1 5 10
117 <210> SEQ ID NO: 16
118 <211> LENGTH: 10
E--> 119 <212> TYPE: Peptide
120 <213> ORGANISM: Artificial sequence
W--> 121 <220> FEATURE:
W--> 121 <223> OTHER INFORMATION:
E--> 121 <400> SEQUENCE: Met Asp Val Phe Met Lys Gly Leu Ser Met
122 1 5 10

```

RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/509,095

DATE: 10/04/2004

TIME: 11:05:10

Input Set : A:\PTO.FG.txt

Output Set: N:\CRF4\10042004\J509095.raw

124 <210> SEQ ID NO: 17
125 <211> LENGTH: 9
E--> 126 <212> TYPE: Peptide
127 <213> ORGANISM: Artificial sequence
W--> 128 <220> FEATURE:
W--> 128 <223> OTHER INFORMATION:
E--> 128 <400> SEQUENCE: Met Asp Val Phe Met Lys Gly Leu Ser
129 1 5
131 <210> SEQ ID NO: 18
132 <211> LENGTH: 8
E--> 133 <212> TYPE: Peptide
134 <213> ORGANISM: Artificial sequence
W--> 135 <220> FEATURE:
W--> 135 <223> OTHER INFORMATION:
E--> 135 <400> SEQUENCE: Met Asp Val Phe Met Lys Gly Leu
136 1 5
138 <210> SEQ ID NO: 19
139 <211> LENGTH: 7
E--> 140 <212> TYPE: Peptide
141 <213> ORGANISM: Artificial sequence
W--> 142 <220> FEATURE:
W--> 142 <223> OTHER INFORMATION:
E--> 142 <400> SEQUENCE: Met Asp Val Phe Met Lys Gly
143 1 5
145 <210> SEQ ID NO: 20
146 <211> LENGTH: 6
E--> 147 <212> TYPE: Peptide
148 <213> ORGANISM: Artificial sequence
W--> 149 <220> FEATURE:
W--> 149 <223> OTHER INFORMATION:
E--> 149 <400> SEQUENCE: Met Asp Val Phe Met Lys
150 1 5

same
error



The types of errors shown exist throughout the Sequence Listing. Please check subsequent sequences for similar errors.

see sample sequence (attached
in back) for valid format
Also, please consult Sequence Rules

RAW SEQUENCE LISTING ERROR SUMMARY
PATENT APPLICATION: US/10/509,095

DATE: 10/04/2004
TIME: 11:05:11

*err
Explanation*
Input Set : A:\PTO.FG.txt
Output Set: N:\CRF4\10042004\J509095.raw

Use of <220> Feature (NEW RULES):

Sequence(s) __ are missing the <220> Feature and associated headings.

Use of <220> to <223> is MANDATORY if <213> ORGANISM is "Artificial Sequence" or "Unknown". Please explain source of genetic material in <220> to <223> section (See "Federal Register," 6/01/98, Vol. 63, No. 104, pp.29631-32) (Sec.1.823 of new Rules)

Seq#:1,2,3,4,5,6,7,8,9,10,11,12,13,14,15,16,17,18,19,20,21,22,23,24,25,26,27
Seq#:28,29,30,31,32,33,34,35,36,37,38,39,40,41,42,43,44,45,46

10/509,095

6

These
are
prior
data

SEQUENCE LISTING

Sequence Protocol

<110> JSW RESEARCH FORSCHUNGSLABOR GMBH

<120> Neurotrophic and Neuroprotective Peptides

<150> <140> PCT/AT/03/00065

<151> <141> 3/10/2003 2003-03-10

<150> AT A 495/2002

<151> 3/28/2002 2002-03-28

use this format for dates

<110> Smith, John; Smithgene Inc.

<120> Example of a Sequence Listing

<130> 01-00001

<140> PCT/EP98/00001

<141> 1998-12-31

<150> US 08/999,999

<151> 1997-10-15

<160> 4

<170> PatentIn version 2.0

<210> 1

<211> 389

<212> DNA

<213> Paramecium sp.

<220>

<221> CDS

<222> (279)...(389)

<300>

<301> Doe, Richard

<302> Isolation and Characterization of a Gene Encoding a
Protease from Paramecium sp.

<303> Journal of Genes

<304> 1

<305> 4

<306> 1-7

<307> 1988-06-31

<308> 123456

<309> 1988-06-31

<400> 1

agctgtagtc	attcctgtgt	cctcttctct	ctgggcttct	caccctgcta	atcagatctc	60
agggagagtg	tcttgaccct	cctctgcctt	tgcagcttca	caggcaggca	ggcaggcagc	120
tgatgtggca	attgctggca	gtgccacagg	cttttcagcc	aggcttaggg	tgggttcgc	180
cgcggcgcgg	cggccctct	cgcgctctc	tcgcgcctct	ctctcgctct	cctctcgctc	240

Consult this

ggacctgatt	aggtgagcag	gaggaggggg	cagtttagc	atg Met 1	ggt Val	tca Ser	atg Met	ttc Phe 5	agc Ser	296						
ttg Leu	tct Ser	ttc Phe	aaa Lys 10	tgg Trp	cct Pro	gga Gly	ttt Phe	tgt Cys 15	ttg Leu	ttt Phe	ggt Val	tgt Cys	ttg Leu 20	ttc Phe	caa Gln	344
tgt Cys	ccc Pro	aaa Lys 25	gtc Val	ctc Leu	ccc Pro	tgt Cys	cac His 30	tca Ser	tca Ser	ctg Leu	cag Gln	ccg Pro 35	aat Asn	ctt Leu	389	
<210>	2															
<211>	37															
<212>	PRT															
<213>	Paramecium sp.															
<400>	2															
Met 1	Val	Ser	Met	Phe 5	Ser	Leu	Ser	Phe	Lys 10	Trp	Pro	Gly	Phe	Cys 15	Leu	
Phe	Val	Cys	Leu 20	Phe	Gln	Cys	Pro	Lys 25	Val	Leu	Pro	Cys	His 30	Ser	Ser	
Leu	Gln	Pro 35	Asn	Leu												
<210>	3															
<211>	11															
<212>	PRT															
<213>	Artificial Sequence															
<220>																
<223>	Designed peptide based on size and polarity to act as a linker between the alpha and beta chains of Protein XYZ.															
<400>	3															
Met 1	Val	Asn	Leu	Glu 5	Pro	Met	His	Thr	Glu 10	Ile						
<210>	4															
<400>	4															
000																

[Annex VIII follows]

VERIFICATION SUMMARY

PATENT APPLICATION: US/10/509,095

DATE: 10/04/2004

TIME: 11:05:11

Input Set : A:\PTO.FG.txt

Output Set: N:\CRF4\10042004\J509095.raw

L:4 M:283 W: Missing Blank Line separator, <120> field identifier
 L:5 M:283 W: Missing Blank Line separator, <140> field identifier
 L:0 M:201 W: Mandatory field data missing, <130> FILE REFERENCE
 L:5 M:270 C: Current Application Number differs, Replaced Current Application Number
 L:6 M:271 C: Current Filing Date differs, Replaced Current Filing Date
 L:8 M:256 W: Invalid Numeric Header Field, Wrong Prior FILING DATE:YYYY-MM-DD
 L:9 M:283 W: Missing Blank Line separator, <160> field identifier
 L:14 M:310 E: (3) Wrong or Missing Sequence Type, TYPE:
 L:16 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ#:0, <213>
 ORGANISM:Artificial sequence
 L:16 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:0, <213>
 ORGANISM:Artificial sequence
 L:16 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:1 differs:0
 L:16 M:283 W: Missing Blank Line separator, <400> field identifier
 L:16 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:1,Line#:16
 L:21 M:310 E: (3) Wrong or Missing Sequence Type, TYPE:
 L:23 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ#:0, <213>
 ORGANISM:Artificial sequence
 L:23 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:0, <213>
 ORGANISM:Artificial sequence
 L:23 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:2 differs:0
 L:23 M:283 W: Missing Blank Line separator, <400> field identifier
 L:23 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:2,Line#:23
 L:28 M:310 E: (3) Wrong or Missing Sequence Type, TYPE:
 L:30 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ#:0, <213>
 ORGANISM:Artificial sequence
 L:30 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:0, <213>
 ORGANISM:Artificial sequence
 L:30 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:3 differs:0
 L:30 M:283 W: Missing Blank Line separator, <400> field identifier
 L:30 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:3,Line#:30
 L:35 M:310 E: (3) Wrong or Missing Sequence Type, TYPE:
 L:37 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ#:0, <213>
 ORGANISM:Artificial sequence
 L:37 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:0, <213>
 ORGANISM:Artificial sequence
 L:37 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:4 differs:0
 L:37 M:283 W: Missing Blank Line separator, <400> field identifier
 L:37 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:4,Line#:37
 L:42 M:310 E: (3) Wrong or Missing Sequence Type, TYPE:
 L:44 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ#:0, <213>
 ORGANISM:Artificial sequence
 L:44 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:0, <213>
 ORGANISM:Artificial sequence
 L:44 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:5 differs:0
 L:44 M:283 W: Missing Blank Line separator, <400> field identifier
 L:44 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:5,Line#:44
 L:49 M:310 E: (3) Wrong or Missing Sequence Type, TYPE:
 L:51 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ#:0, <213>
 ORGANISM:Artificial sequence
 L:51 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:0, <213>
 ORGANISM:Artificial sequence
 L:51 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:6 differs:0

L:51 M:283 W: Missing Blank Line separator, <400> field identifier
L:51 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:6,Line#:51
L:56 M:310 E: (3) Wrong or Missing Sequence Type, TYPE:
L:58 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ#:0, <213>
ORGANISM:Artificial sequence
L:58 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:0, <213>
ORGANISM:Artificial sequence
L:58 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:7 differs:0
L:58 M:283 W: Missing Blank Line separator, <400> field identifier

VERIFICATION SUMMARY

PATENT APPLICATION: US/10/509,095

DATE: 10/04/2004

TIME: 11:05:11

Input Set : A:\PTO.FG.txt

Output Set: N:\CRF4\10042004\J509095.raw

L:58 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:7,Line#:58
L:63 M:310 E: (3) Wrong or Missing Sequence Type, TYPE:
L:65 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ#:0, <213>
ORGANISM:Artificial sequence
L:65 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:0, <213>
ORGANISM:Artificial sequence
L:65 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:8 differs:0
L:65 M:283 W: Missing Blank Line separator, <400> field identifier
L:65 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:8,Line#:65
L:70 M:310 E: (3) Wrong or Missing Sequence Type, TYPE:
L:72 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ#:0, <213>
ORGANISM:Artificial sequence
L:72 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:0, <213>
ORGANISM:Artificial sequence
L:72 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:9 differs:0
L:72 M:283 W: Missing Blank Line separator, <400> field identifier
L:72 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:9,Line#:72
L:77 M:310 E: (3) Wrong or Missing Sequence Type, TYPE:
L:79 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ#:0, <213>
ORGANISM:Artificial sequence
L:79 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:0, <213>
ORGANISM:Artificial sequence
L:79 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:10 differs:0
L:79 M:283 W: Missing Blank Line separator, <400> field identifier
L:79 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:10,Line#:79
L:84 M:310 E: (3) Wrong or Missing Sequence Type, TYPE:
L:86 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ#:0, <213>
ORGANISM:Artificial sequence
L:86 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:0, <213>
ORGANISM:Artificial sequence
L:86 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:11 differs:0
L:86 M:283 W: Missing Blank Line separator, <400> field identifier
L:86 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:11,Line#:86
L:91 M:310 E: (3) Wrong or Missing Sequence Type, TYPE:
L:93 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ#:0, <213>
ORGANISM:Artificial sequence
L:93 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:0, <213>
ORGANISM:Artificial sequence
L:93 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:12 differs:0
L:93 M:283 W: Missing Blank Line separator, <400> field identifier
L:93 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:12,Line#:93
L:98 M:310 E: (3) Wrong or Missing Sequence Type, TYPE:
L:100 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ#:0, <213>
ORGANISM:Artificial sequence
L:100 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:0, <213>
ORGANISM:Artificial sequence
L:100 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:13 differs:0
L:100 M:283 W: Missing Blank Line separator, <400> field identifier
L:100 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:13,Line#:100
L:105 M:310 E: (3) Wrong or Missing Sequence Type, TYPE:
L:107 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ#:0, <213>
ORGANISM:Artificial sequence
L:107 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:0, <213>

ORGANISM:Artificial sequence

L:107 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:14 differs:0

L:107 M:283 W: Missing Blank Line separator, <400> field identifier

L:107 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:14,Line#:107

L:112 M:310 E: (3) Wrong or Missing Sequence Type, TYPE:

L:114 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ#:0, <213>

ORGANISM:Artificial sequence

L:114 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:0, <213>

ORGANISM:Artificial sequence

L:114 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:15 differs:0

L:114 M:283 W: Missing Blank Line separator, <400> field identifier

L:114 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:15,Line#:114

VERIFICATION SUMMARY

PATENT APPLICATION: US/10/509,095

DATE: 10/04/2004

TIME: 11:05:11

Input Set : A:\PTO.FG.txt

Output Set: N:\CRF4\10042004\J509095.raw

L:119 M:310 E: (3) Wrong or Missing Sequence Type, TYPE:
L:121 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ#:0, <213>
ORGANISM:Artificial sequence
L:121 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:0, <213>
ORGANISM:Artificial sequence
L:121 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:16 differs:0
L:121 M:283 W: Missing Blank Line separator, <400> field identifier
L:121 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:16,Line#:121
L:126 M:310 E: (3) Wrong or Missing Sequence Type, TYPE:
L:128 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ#:0, <213>
ORGANISM:Artificial sequence
L:128 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:0, <213>
ORGANISM:Artificial sequence
L:128 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:17 differs:0
L:128 M:283 W: Missing Blank Line separator, <400> field identifier
L:133 M:310 E: (3) Wrong or Missing Sequence Type, TYPE:
L:135 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:18 differs:0
L:135 M:283 W: Missing Blank Line separator, <400> field identifier
L:140 M:310 E: (3) Wrong or Missing Sequence Type, TYPE:
L:142 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:19 differs:0
L:142 M:283 W: Missing Blank Line separator, <400> field identifier
L:147 M:310 E: (3) Wrong or Missing Sequence Type, TYPE:
L:149 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:20 differs:0
L:149 M:283 W: Missing Blank Line separator, <400> field identifier
L:154 M:310 E: (3) Wrong or Missing Sequence Type, TYPE:
L:156 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:21 differs:0
L:156 M:283 W: Missing Blank Line separator, <400> field identifier
L:161 M:310 E: (3) Wrong or Missing Sequence Type, TYPE:
L:163 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:22 differs:0
L:163 M:283 W: Missing Blank Line separator, <400> field identifier
L:168 M:310 E: (3) Wrong or Missing Sequence Type, TYPE:
L:170 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:23 differs:0
L:170 M:283 W: Missing Blank Line separator, <400> field identifier
L:175 M:310 E: (3) Wrong or Missing Sequence Type, TYPE:
L:177 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:24 differs:0
L:177 M:283 W: Missing Blank Line separator, <400> field identifier
L:182 M:310 E: (3) Wrong or Missing Sequence Type, TYPE:
L:184 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:25 differs:0
L:184 M:283 W: Missing Blank Line separator, <400> field identifier
L:189 M:310 E: (3) Wrong or Missing Sequence Type, TYPE:
L:191 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:26 differs:0
L:191 M:283 W: Missing Blank Line separator, <400> field identifier
L:196 M:310 E: (3) Wrong or Missing Sequence Type, TYPE:
L:198 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:27 differs:0
L:198 M:283 W: Missing Blank Line separator, <400> field identifier
L:203 M:310 E: (3) Wrong or Missing Sequence Type, TYPE:
L:205 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:28 differs:0
L:205 M:283 W: Missing Blank Line separator, <400> field identifier
L:210 M:310 E: (3) Wrong or Missing Sequence Type, TYPE:
L:212 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:29 differs:0
L:212 M:283 W: Missing Blank Line separator, <400> field identifier
L:217 M:310 E: (3) Wrong or Missing Sequence Type, TYPE:
L:219 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:30 differs:0

VERIFICATION SUMMARY

PATENT APPLICATION: US/10/509,095

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TIME: 11:05:11

Input Set : A:\PTO.FG.txt

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L:219 M:283 W: Missing Blank Line separator, <400> field identifier
L:224 M:310 E: (3) Wrong or Missing Sequence Type, TYPE:
L:226 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:31 differs:0
L:226 M:283 W: Missing Blank Line separator, <400> field identifier
L:231 M:310 E: (3) Wrong or Missing Sequence Type, TYPE:
L:233 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:32 differs:0
L:233 M:283 W: Missing Blank Line separator, <400> field identifier
L:237 M:310 E: (3) Wrong or Missing Sequence Type, TYPE:
L:239 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:33 differs:0
L:239 M:283 W: Missing Blank Line separator, <400> field identifier
L:244 M:310 E: (3) Wrong or Missing Sequence Type, TYPE:
L:246 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:34 differs:0
L:246 M:283 W: Missing Blank Line separator, <400> field identifier
L:251 M:310 E: (3) Wrong or Missing Sequence Type, TYPE:
L:253 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:35 differs:0
L:253 M:283 W: Missing Blank Line separator, <400> field identifier
L:258 M:310 E: (3) Wrong or Missing Sequence Type, TYPE:
L:260 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:36 differs:0
L:260 M:283 W: Missing Blank Line separator, <400> field identifier
L:265 M:310 E: (3) Wrong or Missing Sequence Type, TYPE:
L:267 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:37 differs:0
L:267 M:283 W: Missing Blank Line separator, <400> field identifier
L:272 M:310 E: (3) Wrong or Missing Sequence Type, TYPE:
L:274 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:38 differs:0
L:274 M:283 W: Missing Blank Line separator, <400> field identifier
L:279 M:310 E: (3) Wrong or Missing Sequence Type, TYPE:
L:281 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:39 differs:0
L:281 M:283 W: Missing Blank Line separator, <400> field identifier
L:286 M:310 E: (3) Wrong or Missing Sequence Type, TYPE:
L:288 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:40 differs:0
L:288 M:283 W: Missing Blank Line separator, <400> field identifier
L:293 M:310 E: (3) Wrong or Missing Sequence Type, TYPE:
L:295 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:41 differs:0
L:295 M:283 W: Missing Blank Line separator, <400> field identifier
L:300 M:310 E: (3) Wrong or Missing Sequence Type, TYPE:
L:302 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:42 differs:0
L:302 M:283 W: Missing Blank Line separator, <400> field identifier
L:307 M:310 E: (3) Wrong or Missing Sequence Type, TYPE:
L:309 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:43 differs:0
L:309 M:283 W: Missing Blank Line separator, <400> field identifier
L:314 M:310 E: (3) Wrong or Missing Sequence Type, TYPE:
L:316 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:44 differs:0
L:316 M:283 W: Missing Blank Line separator, <400> field identifier
L:321 M:310 E: (3) Wrong or Missing Sequence Type, TYPE:
L:323 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:45 differs:0
L:323 M:283 W: Missing Blank Line separator, <400> field identifier
L:328 M:310 E: (3) Wrong or Missing Sequence Type, TYPE:
L:330 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:46 differs:0
L:330 M:283 W: Missing Blank Line separator, <400> field identifier